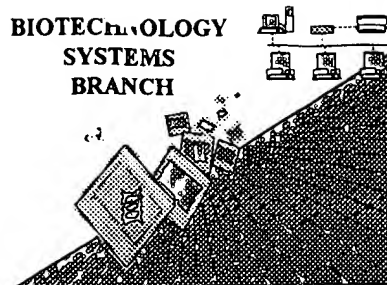


**RAW SEQUENCE LISTING**  
**ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/903,327  
Source: OIPF  
Date Processed by STIC: 7/24/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/903,327

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1. Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2. Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
3. Misaligned Amino Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4. Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5. Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6. PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7. Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8. Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000
9. Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10. Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11. Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12. PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/903,327

DATE: 07/24/2001  
TIME: 11:08:21

Input Set : A:\es.txt  
Output Set: N:\CRF3\07242001\I903327.raw

*pp 2, 4-6*  
Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Nemerow, Glen R.  
4 Li, Erguang  
6 <120> TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR  
TARGETED  
7 GENE  
8 DELIVERY  
10 <130> FILE REFERENCE: 22908-1228  
*de* 12 <140> CURRENT APPLICATION NUMBER: US/09/903,327  
13 <141> CURRENT FILING DATE: 2001-07-10  
15 <150> PRIOR APPLICATION NUMBER: ~~converted to a provisional from~~ 09/613,017  
16 <151> PRIOR FILING DATE: 2000-07-10  
18 <160> NUMBER OF SEQ ID NOS: 33  
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0

## ERRORED SEQUENCES

22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 1516  
24 <212> TYPE: DNA  
25 <213> ORGANISM: Mouse  
27 <220> FEATURE:  
28 <221> NAME/KEY: CDS  
29 <222> LOCATION: (28)...(1395)  
30 <223> OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody  
32 <400> SEQUENCE: 1  
33 cagacactga acacactgac tctaacc atg gga tgg agc tgg atc ttt ctc ttc 54  
34 Met Gly Trp Ser Trp Ile Phe Leu Phe  
35 1 5  
37 ctc ctg tca gga act gca ggc gtc cac tct gag gtc cag ctt cag cag 102  
38 Leu Leu Ser Gly Thr Ala Gly Val His Ser Glu Val Gln Leu Gln Gln  
39 10 15 20 25  
41 tca gga cct gag ctg gtg aaa cct ggg gcc tca gtg aag ata tcc tgc 150  
42 Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys  
43 30 35 40  
45 aag gct tct gga tac aca ttc act gac tac aac atg cac tgg gtg aag 198  
46 Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met His Trp Val Lys  
47 45 50 55  
49 cag agc cat gga aag agc ctt gag tgg att gga tat att tat cct tac 246  
50 Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr  
51 60 65 70  
53 aaa ggt ggt act ggc tac aac cag aag ttc aag agc aag gcc aca ttg 294  
54 Lys Gly Gly Thr Gly Tyr Asn Gln Lys Phe Lys Ser Lys Ala Thr Leu  
55 75 80 85  
57 aca aca gac agt tcc tcc aac aca gcc tac atg gag ctc cgc agc ctg 342  
58 Thr Thr Asp Ser Ser Asn Thr Ala Tyr Met Glu Leu Arg Ser Leu  
59 90 95 100 105  
61 aca tct gat gcc tct gca gtc tat tac tgt gca aga ggg att gct tac 390

## RAW SEQUENCE LISTING

DATE: 07/24/2001

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TIME: 11:08:21

Input Set : A:\es.txt

Output Set: N:\CRF3\07242001\I903327.raw

```

62 Thr Ser Asp Ala Ser Ala Val Tyr Tyr Cys Ala Arg Gly Ile Ala Tyr
63          110          115          120
65 tgg ggc caa ggg act ctg gtc act gtc tct gca gcc aaa acg aca ccc      438
66 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro
67          125          130          135
69 cca tct gtc tat cca ctg gcc cct gga tct gct gcc caa act aac tcc      486
70 Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
71          140          145          150
73 atg gtg acc ctg gga tgc ctg gtc aag ggc tat ttc cct gag cca gtg      534
74 Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
75          155          160          165
77 aca gtg acc tgg aac tct gga tcc ctg tcc agc ggt gtg cac acc ttc      582
78 Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
79 170          175          180          185
81 cca gct gtc ctg cag tct gac ctc tac act ctg agc agc tca gtg act      630
82 Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
83          190          195          200
85 gtc ccc tcc agc acc tgg ccc agc gag acc gtc acc tgc aac gtt gcc      678
86 Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
87          205          210          215
89 cac ccg gcc agc agc acc aag gtg gac aag aaa att gtg ccc agg gat      726
90 His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
91          220          225          230
E--> 93 tgt ggt tgt aag cct tgc ata tgt aca gtc cca gaa gta tca tct gtc
94 Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
95          235          240          245
97 ttc atc ttc ccc cca aag ccc aag gat gtg ctc acc att act ctg act      822
98 Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
99 250          255          260          265
101 cct aag gtc acg tgt gtt gtg gta gac atc agc aag gat gat ccc gag      870
102 Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu
103          270          275          280
105 gtc cag ttc agc tgg ttt gta gat gat gtg gag gtg cac aca gct cag      918
106 Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
107          285          290          295
109 acg caa ccc ccg gag gag cag ttc aac agc act ttc cgc tca gtc agt      966
110 Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
111          300          305          310
113 gaa ctt ccc atc atg cac cag gac tgg ctc aat ggc aag gag ttc aaa      1014
114 Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
115          315          320          325
117 tgc agg gtc aac agt gca gct ttc cct gcc ccc atc gag aaa acc atc      1062
118 Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile
119 330          335          340          345
121 tcc aaa acc aaa ggc aga ccg aag gct cca cag gtg tac acc att cca      1110
122 Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro
123          350          355          360
125 cct ccc aag gag cag atg gcc aag gat aaa gtc agt ctg acc tgc atg      1158
126 Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met

```

(765) 774

## RAW SEQUENCE LISTING

DATE: 07/24/2001

PATENT APPLICATION: US/09/903,327

TIME: 11:08:21

Input Set : A:\es.txt

Output Set: N:\CRF3\07242001\I903327.raw

```

127          365          370          375
129 ata aca gac ttc ttc cct gaa gac att act gtg gag tgg cag tgg aat      1206
130 Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
131          380          385          390
133 ggg cag cca gcg gag aac tac aag aac act cag ccc atc atg gac aca      1254
134 Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
135          395          400          405
137 gat ggc tct tac ttc gtc tac agc aag ctc aat gtg cag aag agc aac      1302
138 Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
139 410          415          420          425
141 tgg gag gca gga aat act ttc atc tgc tct gtg tta cat gag ggc ctg      1350
142 Trp Glu Ala Gly Asn Thr Phe Ile Cys Ser Val Leu His Glu Gly Leu
143          430          435          440
145 cac aac cac cat act gag aag agc ctc tcc cac tct cct ggt aaa      1395
146 His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
147          445          450          455
149 tgateccagt gtccttggag ccctctgggc ctacaggact ctgtcaccta cctccacccc      1455
150 tccctgtata aataaagcac cttagcactgc cttgggaccc tgcaataaaaa aaaaaaaaaa      1515
151 a      1516

```

735 &lt;210&gt; SEQ ID NO: 12

736 &lt;211&gt; LENGTH: 510

737 &lt;212&gt; TYPE: PRT

738 &lt;213&gt; ORGANISM: Artificial Sequence

740 &lt;220&gt; FEATURE:

741 <223> OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain  
 742 and IGF-1 mature peptide

744 &lt;400&gt; SEQUENCE: 12

```

745 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
746 1          5          10          15
747 Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
748          20          25          30
749 Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
750          35          40          45
751 Thr Asp Tyr Asn Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu
752          50          55          60
753 Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Lys Gly Gly Thr Gly Tyr Asn
754 65          70          75          80
755 Gln Lys Phe Lys Ser Lys Ala Thr Leu Thr Thr Asp Ser Ser Ser Asn
756          85          90          95
757 Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Asp Ala Ser Ala Val
758          100          105          110
759 Tyr Tyr Cys Ala Arg Gly Ile Ala Tyr Trp Gly Gln Gly Thr Leu Val
760          115          120          125
761 Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala
762          130          135          140
763 Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu
764 145          150          155          160
765 Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly
766          165          170          175

```

## RAW SEQUENCE LISTING

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Input Set : A:\es.txt

Output Set: N:\CRF3\07242001\I903327.raw

```

767 Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp
768      180      185      190
769 Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro
770      195      200      205
771 Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys
772      210      215      220
773 Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile
774 225      230      235      240
775 Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro
776      245      250      255
777 Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val
778      260      265      270
779 Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val
780      275      280      285
781 Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln
782      290      295      300
783 Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln
784 305      310      315      320
785 Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala
786      325      330      335
787 Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro
788      340      345      350
789 Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala
790      355      360      365
791 Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu
792      370      375      380
793 Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr
794 385      390      395      400
795 Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr
796      405      410      415
797 Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe
798      420      425      430
799 Ile Cys Ser Val Leu His Glu Phe Gly Pro Glu Thr Leu Cys Gly Ala
800      435      440      445
801 Glu Leu Val Asp Ala Leu Gln Phe Val Cys Gly Asp Arg Gly Phe Tyr
802      450      455      460
803 Phe Asn Lys Pro Thr Gly Tyr Gly Ser Ser Ser Arg Arg Ala Pro Gln
804 465      470      475      480
805 Thr Gly Ile Val Asp Glu Cys Cys Phe Arg Ser Cys Asp Leu Arg Arg
806      485      490      495
807 Leu Glu Met Tyr Cys Ala Pro Leu Lys Pro Ala Lys Ser Ala

```

E--&gt; 808 500 505

*510 ← insert number*

1156 &lt;210&gt; SEQ ID NO: 30

1157 &lt;211&gt; LENGTH: 96

1158 &lt;212&gt; TYPE: DNA

1159 &lt;213&gt; ORGANISM: Artificial Sequence

1161 &lt;220&gt; FEATURE:

1162 &lt;223&gt; OTHER INFORMATION: PCR sense primer for subcloning EGF into DAV-1/EGF

1163 fusion construct.

*next page*

## RAW SEQUENCE LISTING

DATE: 07/24/2001

PATENT APPLICATION: US/09/903,327

TIME: 11:08:21

Input Set : A:\es.txt

Output Set: N:\CRF3\07242001\I903327.raw

1165 <400> SEQUENCE: 30  
E--> 1166 gaattcaata gtgactctga atgtcccctg tcccacgatg ggtactgctt ccatgatggt 60  
1167 60  
1168 gtgtgcatgt atattgaagc attggacaag tatgca 96  
1170 <210> SEQ ID NO: 31  
1171 <211> LENGTH: 98  
1172 <212> TYPE: DNA  
1173 <213> ORGANISM: Artificial Sequence  
1175 <220> FEATURE:  
1176 <223> OTHER INFORMATION: PCR antisense primer for subcloning EGF into DAV-1/EGF  
1177 fusion construct.  
1179 <400> SEQUENCE: 31  
E--> 1180 gaattctagc gcagttccca ccacttcagg tctcggtact gacatcgctc cccgatgtag 60  
1181 60  
1182 ccaacaacac agttgcatgc atacttgctc aatgcttc 98

*format error*  
*see*  
*Item 1*  
*on Error*  
*summary sheet*

*same*  
*error*

<210> 5  
<211> 1314  
<212> DNA  
<213> Mouse

*coding region begins with base at location 1*

<220>  
<221> CDS (1)  
<222> (0) .. (1314)

<223> Portion of DAV-1 heavy chain used for fusion protein  
bifunctional antibody

<400> 5

atg gga tgg agc tgg atc ttt ctc ttc ctc ctg tca gga act gca ggc 48  
Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly  
1 5 10 15



**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/903,327

DATE: 07/24/2001

TIME: 11:08:22

Input Set : A:\es.txt

Output Set: N:\CRF3\07242001\I903327.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:93 M:254 E: No. of Bases conflict, LENGTH:Input:765 Counted:774 SEQ:1  
L:350 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:5, CDS LOCATION: (0)...  
(1314)  
L:808 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12  
L:1166 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:30  
L:1180 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:31